

AGATGATGT CCGCGGTGCA AGGTGCAAGT TCGCGGCAT
 METSerVal GlyArgArg ArgValLysLeu LeuGlyIle
 1 CCGTATGATG GCGAAATGCT TCATTATTT CATTGTGGA
 eLeuMETMET AlaAsnValPhe IleTyrLeu IleValGlu
 2 TCTCTAAA ACAGTAGCCA AGCAAAAAT CGAAGGGG
 ValSerLysAsn SerSerGln AspLysAsn GlyLysGlyG
 3 GGTATATAT CCGAAGAG AGGTCTGCA AGCCACCG
 lyValIleIle ProLysGlu LysPheTrpLys ProProSe
 4 CACTCGGCG CACTACTGCA ACAGGGGACA CGAGAAGCT
 ThrProArg AlaTyrTrpAsn ArgGluGln GluLysLeu
 5 AGCGGTGT ACAATCGCT CTTCACAGG GTCGCAATC
 AsnArgProPyr AsnProIle LeuAsnArg ValAlaAsn
 6 AGACGGGCA GCTAGGCA TCTCAACA CAGTCACT
 LysTrpGlyGlu LeuAlaThr SerProAsnThr SerHisLe
 7 CAGCTATCT CAGCAGACT CCGCTCTAT CAGAGCTTG
 eSerTyrCys GluProAspSer ThrValMET ThrAlaVal
 8 ACAGATTTA ATAATCTCC CAGCAGATT AAAGCTTTC
 ThrAspPheAsn AsnLeuPro AspArgPhe LysAspPhe
 9 TCTGTATTT CAGATCGCG AATTACTGC TCTTATAGA
 eLeuTyrLeu ArgCysArg AsnTyrSerLeu LeuIleAs
 10 TCAACCGAG AATGTGCA AGAGCCCTT CTCTATCT
 pGlnProLys LysCysAlaLys LysProPhe LeuLeuLeu
 11 CGATTAAGT CCGTATTC ACATTTTCC AGAAGGCG
 AlaIleLysSer LeuIlePro HisPheAla ArgArgGln
 12 CATTCCGA GTCTCGGC CGCAAAACA AGCTGGGA
 LeuArgGlu SerTrpGly ArgGluThrAsn ValGlyAs
 13 CCGCAGTA GTGCGGTCT TCGCTTGG CAGAGCACC
 nGlnThrVal ValArgValPhe LeuLeuGly LysThrPro
 14 CAGGGACA ACCACCTCA CCGTGGGC ATCGTAACT
 ProGluAspAsn HisProAsp LeuSerAsp METLeuLysP
 15 TTGAGGTGA CAGCACAG CACATCTCA TGTGGACTA
 heGluSerAsp LysHisGln AspIleLeuMET TrpAsnLys
 16 TAGAGACA TTCTCAACC TGTCTGAA CGAGTCTG
 rArgAspThr PhePheAsnLeu SerLeuLys GluValLeu

FIG. 1 (sheet 1 of 2)

541 TTCTTGGT CCGTGGCA TTTGTGCA GAGCAGGT
 PheLeuArgTrp ValSerThr SerCysPro AspAlaGluP
 571 TTGCTTCA GGGGTGAT GAGGTTC TCAACCCA
 LeuValPheLys GlyAspAsp AspValPheVal AsnThrHi
 601 TGCATGCT AATTACTCA ATAGCTATC CAAGGCCAA
 sHisIleLeu AsnTyrLeuAsn SerLeuSer LysSerLys
 631 GCGAAGCT TTTCTATG TGGTGATC CCAATCTG
 AlaLysAspLeu PheIleGly AspValIle HisAsnAlaG
 661 GCGTCAAG GGTAGAAA CTGAGTACT ACATCCAG
 LysProHisArg AspLysLys LeuLysTyrTyr IleProG
 691 AGTCTTCT ACCGCTCT ACCGCTCA TCCCGGGT
 uValPheLys ThrGlyValTyr ProProTyr AlaGlyGly
 721 GGTGATTC TGTATCCG CCGCTTCC TTAGGCTT
 GlyGlyPheLeu TyrSerGly ProLeuAla LeuArgLeuT
 751 ACAGTCCG TCCCGCTC GCTCTTCC CTATTCATC
 TyrSerAlaThr SerArgVal HisLeuTyrPro IleAspAs
 781 TTTTCTAC CCAATGCG TCGAAACT GGGCTTGT
 pValTyrThr GlyMetCysLeu GluLysLeu GlyLeuVal
 811 CTGAGAGC ACAAGGCT CAGCATTT CATATGAG
 ProGluLysHis LysGlyPhe ArgThrPhe AspIleGluG
 841 AGAAAAAT CAAAAAT TTTCTATA TGAAGTAT
 uLysAsnLys LysAsnIle CysSerTyrIle AspLeuME
 871 CTATGACT AGCGAAGC CTCAGAGT GATGATTC
 LeuValHis SerArgLysPro GluGluMET IleAspIle
 901 TGTCTGCT TCGAGTCC TATTAAAA TGTCTA
 TrpSerGluLeu HisSerPro AsnLeuLys Cys

FIG. 1 (sheet 2 of 2)

FIG. 2 (sheet 2 of 2)

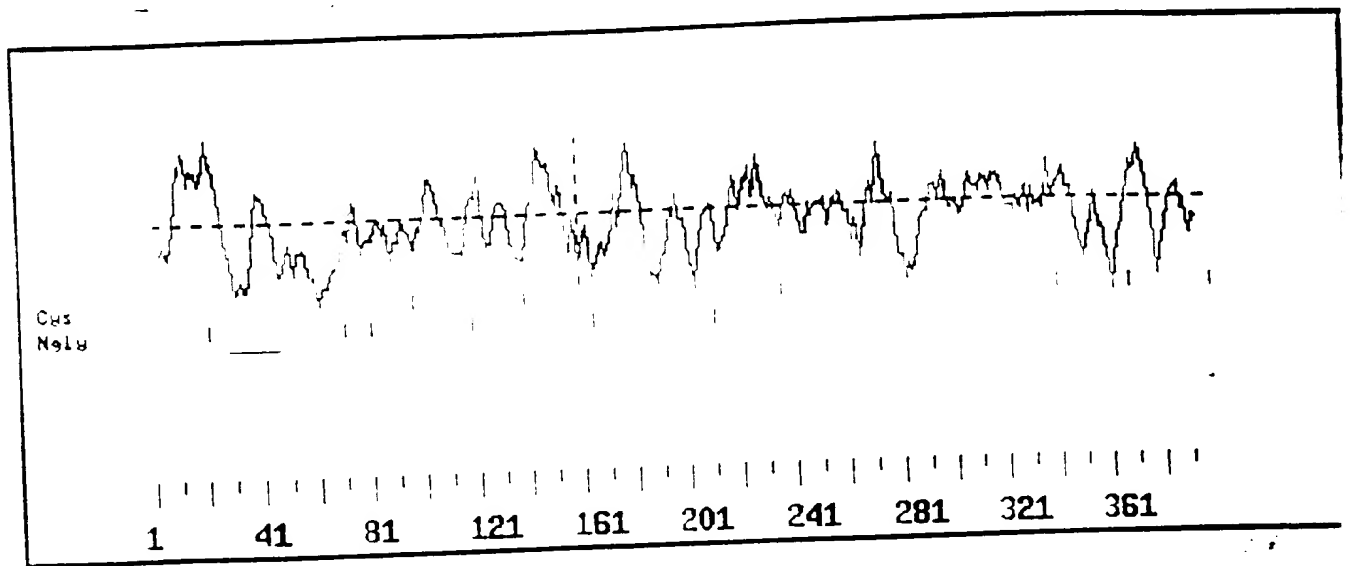


FIG. 3

ATGATTTGCG CTCTGCTTT ACTGGTATT TTAGAAAT
 METIleCysPro SerAlaLeu LeuValIle LeuArgAsnL
 11 TAAATCGCGA AGAAAAATC ATTCTCAG AGATCTCA
 euIleArgGlu GluLysIle IleSerGlnGlu IleLeuAs
 21 TTGATTGAA TTAGGATGA AAAAGCGAA TATTCAGTTC
 nLeuIleGlu LeuArgMETLys LysGlyAsn IleGlnLeu
 31 ACAACTCTG CAATCAGTGA TGCATTAAA GAAATCGTA
 ThrAsnSerAla IleSerAsp AlaLeuLys GluIleAspS
 41 CTAGTGTGCT CAATGTGCT GTACCGCGG AGACCGGATC
 erSerValLeu AsnValAla ValThrGlyGlu ThrGlySe
 51 AGGGAAGTCC AGCTTCATCA ATACCTCGG AGGCATGGG
 rGlyLysSer SerPheIleAsn ThrLeuArg GlyIleGly
 61 AATGAGAAG AAGGTGCGC TAAACTCGG GTGTGGGG
 AsnGluGluGlu GlyAlaAla LysThrGly ValValGluV
 71 TACCATCGA AGACATCA TACAACACC CCATATACC
 alThrMETGlu ArgHisPro TyrLysHisPro AsnIlePr
 81 CATGTGGT TTGTGGAC TCGTGGAT TGGAGCACA
 cAsnValVal PheTyrAspLeu ProGlyIle GlySerThr
 91 AATTTCGAC CAACACTTA CCGGCGAA ATGAAGTTC
 AsnPheProPro AsnThrTyr LeuGluLys METLysPheT
 101 AAGGTACGA TTCTTCATT ATTATTTCG CCGAGGCTT
 yrGluTyrAsp PhePheIle IleIleSerAla ThrArgPh
 11 CAGAAAAAT GATATAGCA TTGCAAGC AATCGCATC
 elysLysAsn AspileAspile AlaLysAla IleSerMET
 121 AAGAAGAGG AATCTGCTT CCGGAGAC AAGGTGGCT
 METLysLysGlu PheTyrPhe ValArgThr LysValAspS
 131 CTGACATAC AATGAGCA CATGCCAAC CTCAACTT
 erAspileThr AsnGluAla AspGlyLysPro GlnThrPh
 141 TGCAGAA AAGGTCTCC AGGACCTCG COTTAAGCT
 eAspLysGlu LysValLeuGln AspileArg LeuAsnOys
 151 CTGACACTT TTAGGGGAA TGGCATTCCT GAGCGCCAA
 ValAsnThrPhe ArgGluAsn GlyIleAla GluProProI
 161 TCTCTCTCT CTCTACAAA AATGTTGTC ACTATGACTT
 lePheLeuLeu SerAsnLys AsnValCysHis TyrAspPh

FIG. 4 (sheet 1 of 2)

581 CCCCCTCTCTC ATGGACAGGC TGTATAGTGA CCCCCTCTATC
 eProValLeu METAspLysLeu IleSerAsp LeuProIle
 591 TCCAGGAGAC ACAATTTTAT CCGTCTCTTA CCGATATCA
 TyrArgArgHis AsnPheMET ValSerLeu ProAsnIleT
 601 CCGATTCCGT CATTCGAAAG AGCCCCAAT TTCTGAGCA
 hrAspSerVal IleGluLys LysArgGlnPhe LeuLysGlu
 611 PGGGTTTGG CCGGAGGGAT TTCTCTCTCA CCGTGTGAAT
 rArgIlePro LeuGluGlyPhe AlaAlaAsp LeuValAsn
 621 ATCATCCCTT CCGTCTCTT TCTCTCTGAC AGTGATTGG
 IleIleProSer LeuIlePhe LeuLeuAsp SerAspLeuG
 631 TCACTCTCA GAAAGCATG AATCTCTCC CCGTCTCTT
 IleIleLeuLys LysSerMET LysPheTyrArg ThrValPhe
 641 TCGAGTCCAT GAAACTCTT TCCAGAGATT AGCTAGGGAC
 eGlyValAsp GluThrSerLeu GluArgLeu AlaArgAsp
 651 TCGGAATAG AGGTCTCTCA CCGGAGGCC ATGATAAAT
 TrpGluIleGlu ValAspGln ValGluAla METIleLysS
 661 CTTCTCTCTT CTTCAAACT ACAGTGGAG AACCAATCA
 erProAlaVal PheLysPro ThrAspGluGlu ThrIleGlu
 671 AGAAGGCTT TCAAGATATA TTGAGGATT CCGTCTCTT
 nGluArgLeu SerArgTyrIle GluGluPhe CysLeuAla
 681 AATGGTACT TACTCTCTTA AATAGTTTT CTTAAGAAA
 AsnGlyTyrLeu LeuProLys AsnSerPhe LeuLysGluI
 691 TATTTCTCT GAAATATAG TCTCTCTCA TCGTCTCTA
 LePheTyrLeu LysTyrTyr PheLeuAspMET ValThrGlu
 701 AGTCTCTAA ACTCTCTTA AGAGATATG TTTPAGAAAC
 AspAlaLys ThrLeuLeuLys GluIleLys LeuArgAsn
 711 PG

FIG. 4 (sheet 2 of 2)

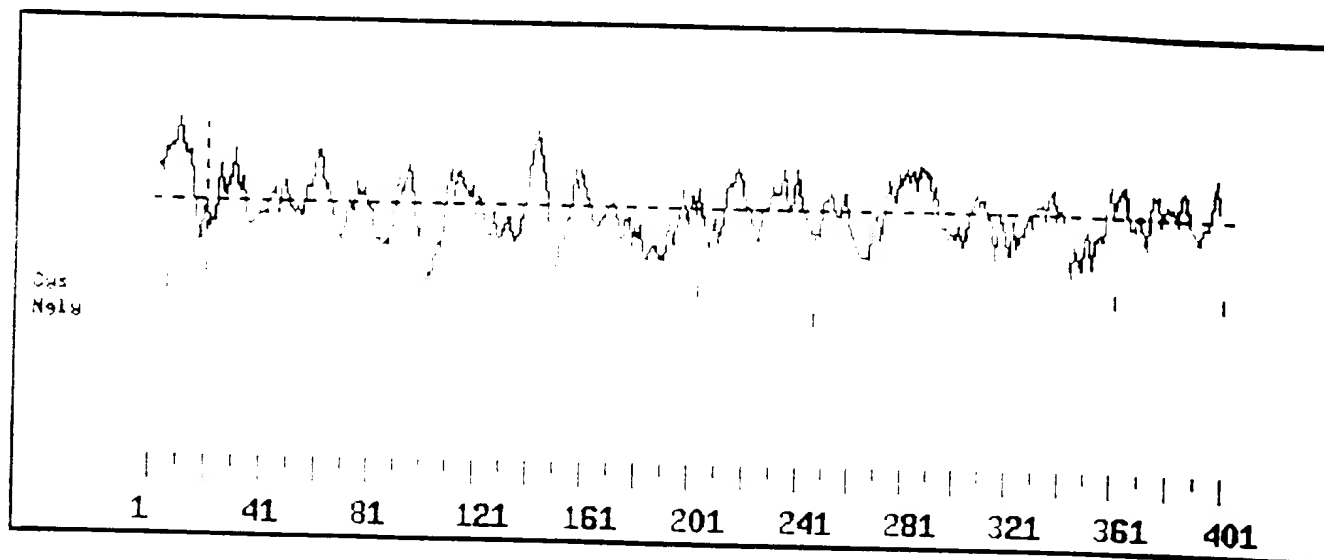


FIG. 5

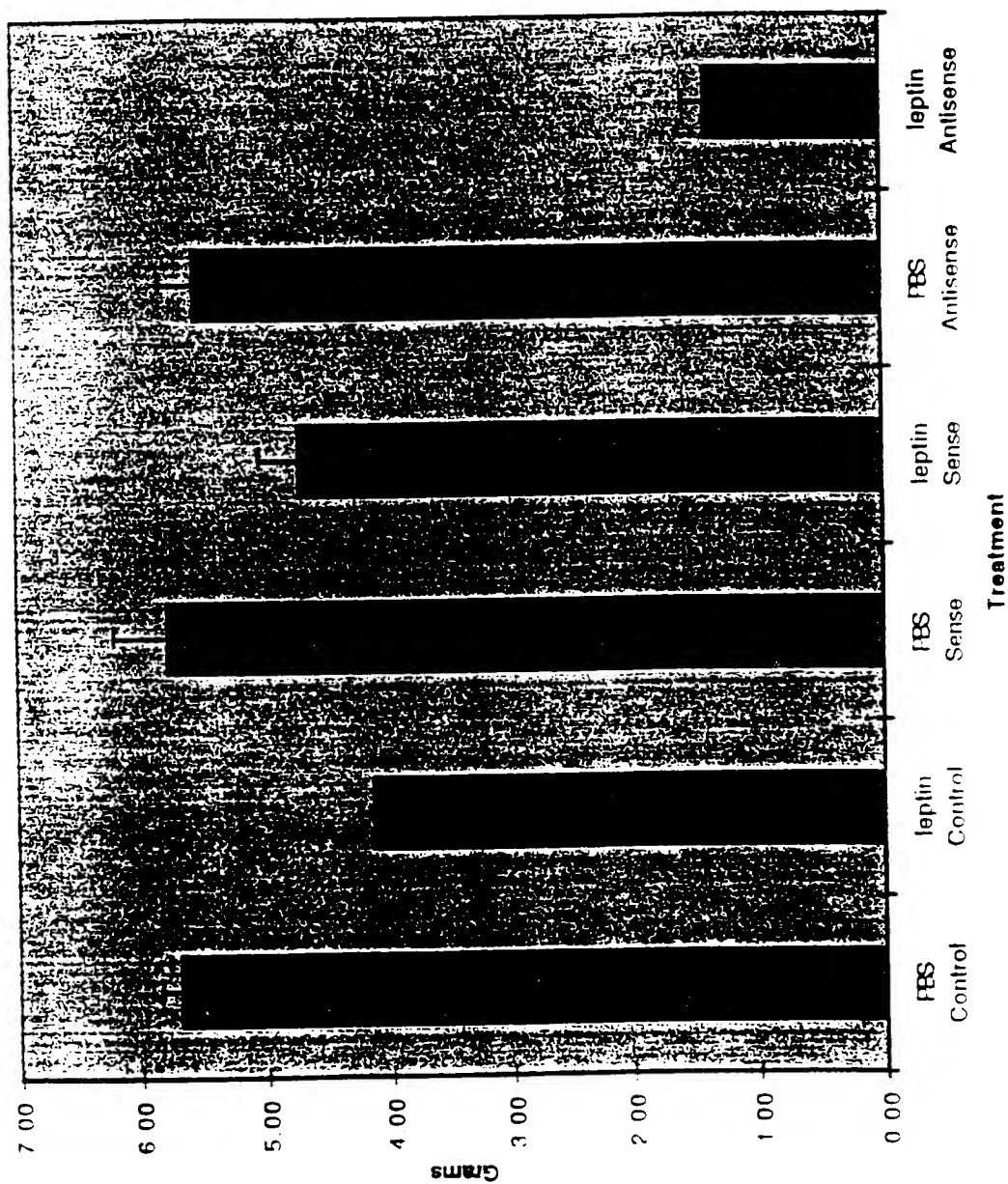


FIG. 6

5'

ACGCGTCCGCGCAGCGGCAGCGGCAGCAGCGGCAACAAGTGCCGGAGGCTA
GCAGAGCCAAGCCGGAGCAGTCCCTGCCGCCGACACCGCCGGGGCCGCCCGTC
CGGGGCGCCGCGCATGGAGCGTGAGCTGCGGCGGTGCGCGGGCTGAGCCGC
GCGGAGCGGCCGGGACGTGGATGTGGCCGCGATCTCCCGCCCTTGCCCCCGC
CCCGCCGAGCTGGAGCTGCTCCCGGACAAGATATGAGAA**ATG**AGTGTTGGA
CGTCGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTA
TTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAAATGGAAAAGGG
GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGG
CATACTGGAACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCT
GAGCATGCTGACCAACCAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAG
CCATCTGAACTACTGCGAACCTGACCTGAGGGGTCACGTCGGTGGTTACGGGT
TTTAACAACCTTGCCGGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGCCG
CAATTATTCACTGCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTTCT
TGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAAGCAATC
CGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGA
GTCTTCCTGCTGGGGCCAGACACCCCCAGAGGACAACCACCCCGACCTTTCAG
ATATGCTGAAATTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACTA
CAGAGACACTTTCTTCAACTTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGG
TAAGTACTTCCTGCCCAGACACTGAGTTTGTTCCTCAAGGGCGATGACGATGTT
TTTGTGAACACCCATCACATCCTGAATTACTTGAATAGTTTATCCAAGACCAA
AGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCTGGACCTCATCGG
GATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTCTACCC
ACCCTATGCAGGGGGAGGGGGGTTCTCTACTCCGGCCACCTGGCCCTGAGG
CTGTACCATATCACTGACCAGGTCCATCTCTACCCCATGATGACGTTTATAC
TGGAATGTGCCTTCAGAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTC

AGGACATTTGATATCGAGGAGAAAAACAAAAATAACATCTGCTCCTATGTAG
ATCTGATGTTAGTACATAGTAGAAAACCTCAAGAGATGATTGATATTTGGTCT
CAGTTGCAGAGTGCTCATTTAAAATGCTAAAATAGATACAAACCTCAATTTKG
SATWGRAAGGGGTWTTTTGRATWGGYCCCATGTTGGGGTCTCACATTAGAGT
AATTTCTATTTNAANCATGAAATTGCCTTTATGAGTGATACCCATTTANGGCC
TCTAANCCTTCATTTGNACTCACGTGAAGAAGGGAAAGCGGGAGAAGGTAAT
TTNTTTATGGTGAATGGCAGGATATTGGTCTGACTTACCGNTAGGGGANTTTA
AAACTGGNCCTTTTTGAATCTGTTTGGATGGCCCTT

MSVGRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPE
AYWNREQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFN
NLPDRFKDFLLYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIREWG
QESNAGNQTVVVRVFLLGQTPPEDNHPDLSMMLKFESEKHQDILMWNRYRDTFFNL
SLKEVLFLRWVSTSCPDTEFVFKGDDDVFNTHHILNYLNSLSKTKAKDLFIGDV
IHNAGPHRDKKLYYIPEVVYSGLYPPYAGGGGFLYSGHLALRLYHITDQVHLY
PIDDVYTGMCCLQKLGLVPEKHKGFRTFDIEEKNKNNICSYVDLMLVHSRKPQEM
IDIWSQLQSAHLKC

START

201 CCCCCCCCCCGGAGCTGGAGCTGCTCCCGGACAAGATATGAGAAATGAGTGTGGSACGT 260
 5 CCCCCCCCCCGGAGCTGGAGGTGTCCCTAGACAAGGTATGAGAGATGAGTGTGGGGCGT 64
 261 CGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTATTTTATTATG 320
 45 CGAAGAGTCAAGTTGCTGGGCATCCTGATGATGGCAAATGTCTTCATTTATTTGATTGTG 124
 321 GAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGGGAAGTAATAATACCCAAA 380
 125 GAAGTCTCCAAAACAGTAGCCAAGACAAAAAATGGAAAGGGAGGAGTAATAATCCCGAAA 184
 381 GAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGGAACCSAGAGCAAGAGAAG 440
 185 GAGAAGTTCTGGAAGCCACCCAGCACTCCCGGGGCATACTGGAACAGGGAACAGGAGAAG 244
 441 CTGAACCSGCAGTACAACCCCATCCTGAGCATGCTGACCAACCAGACCGGGGAGGCGGGC 500
 145 CTGAACAGGTGGTACAATCCCATCTTCAACAGGCTGGCCATCAGACAGGGGAGGTAGCC 564
 561 AGGCTCTCCAATATAAGCCATCTCAACTACTGCGAACCTGACCTCAGGGTCACGTCCGTG 620
 365 AGTCTCTCCAAACACAAAGTCACTGAGCTATTGTGAACCGAGCTCGACGGTCATGACAGCT 684
 621 GTTACGGGTTTTTAACAACCTTGCCCGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGC 620
 365 GTGACAGATTTTAATAATCTGCCCGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGC 684
 621 CGCAATTATTCACTGCTTATAGATCAGCCCGATAAGTGTGCAAAGAAACCTTTCTTGTG 680
 425 CGGAATTACTCGCTGCTTATAGATCAACCCGAAGAAATGTGCAAAGAAGCCCTTCTTACTA 484
 781 CTGGCGATTAAAGTCCCTCACTCCACATTTTGGCAGAAGGCAAGCAATCCGGGAATCCTGG 740
 485 TTGGCGATAAAGTCCCTCATTCCACATTTTGGCAGAAGGCAAGCAATTCGGGAGTCTTGG 844
 741 GGCCAAGAAAGCAACGCAGGGAACCAACCGGTGGTGCGAGTCTTCCTGCTGGGCCAGACA 800
 645 GGCCGAGAAACCAACGTAGGGAACCAGACAGTAGTGAGGGTCTTCCTGTTGGGCAAGACA 604
 801 CCCCCAGAGGACAACCACCCCGACCTTTTCAAGATATGCTGAAATTTGAGAGTGAGAAGCAC 860
 605 CCCCCAGAGGACAACCACCCCTGACCTTTTGGACATGCTTAAGTTTGAGAGTGACAAGCAC 864
 861 CAAGACATTCTTATGTGGAACACAGAGACACTTCTTCAACTGTCTCTGAAGGAAGTG 920
 665 CAGGACATCCTCATGTGGAACATATAGAGACACATTCTTCAACCTGTCCCTGAAGGAAGTG 924
 921 CTGTTTCTCAGGTGGGTAAAGTACTTCTGCCCAGACACTGAGTTTGTCTTCAAGGGCGAT 980
 725 CTGTTTCTTAGGTGGGTGAGCACTTCTCTCCAGACCGAGAGTTTGTCTTCAAGGGCGAT 984
 981 CACGATGTTTTTGTGAACACCCATCAGATCCTGAATTACTTGAATAGTTTATCCAAGAGC 1040
 785 GATGACGTGTTTGTGAACACCCATCAGATCCTTAATTACTTGAATAGCTTATCCAAGAGC 1044
 1041 AAGCCAAAGATCTCTTATAGGTGATGTGATCCCAATGCTGGACCTCTCCGGGATAAG 1100
 845 AAGCCAAAGACTTCTTATAGGTGAGTGTGATCCCAATGCTGGGCTCACCCTGGGATAAG 1104

FIG. 9 (10F2)

MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIIPKEKFWKISTPPEAYWN
MSVGRRRVKLLGILMMANVFIYLIVEVSKNSSQDKNGKGGVIIIPKEKFWKPPSTPRAYWN

REQEKLNRQYNPIELMLTNOTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL
REQEKLNRWYNPIELNRVANQTGELATSPNTSHLSYCEPDSTVMTAVTDFNNLPDRFKDFL

LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVRVF
LYLRCRNYSLIDQPKKCAKKPFLLLAIKSLIPHFARRQAIRESWGRETNGNQTVVRVF

LLGQTPPEDNHPDLSMDLKFESKQDILMWNYRDTFFNLSLKEVLFLRWVSTSCPDTEF
LLGKTPPEDNHPDLSMDLKFESDKQDILMWNYRDTFFNLSLKEVLFLRWVSTSCPDAEF

VFKGDDDDVFVNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYSGLY
VFKGDDDDVFVNTHHILNYLNSLSKSKAKDLFIGDVIHNAGPHRDKKLYYIPEVFYTGvy

PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTGMLQKLGLVPEKHKGFRTFDIEE
PPYAGGGGFLYSGPLALRLYSATSRVHLYPIDDVYTGMLQKLGLVPEKHKGFRTFDIEE

KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC
KNKNNICSYIDLMLVHSRKPQEMIDIWSQLQSPNLKC

FIG. 11

